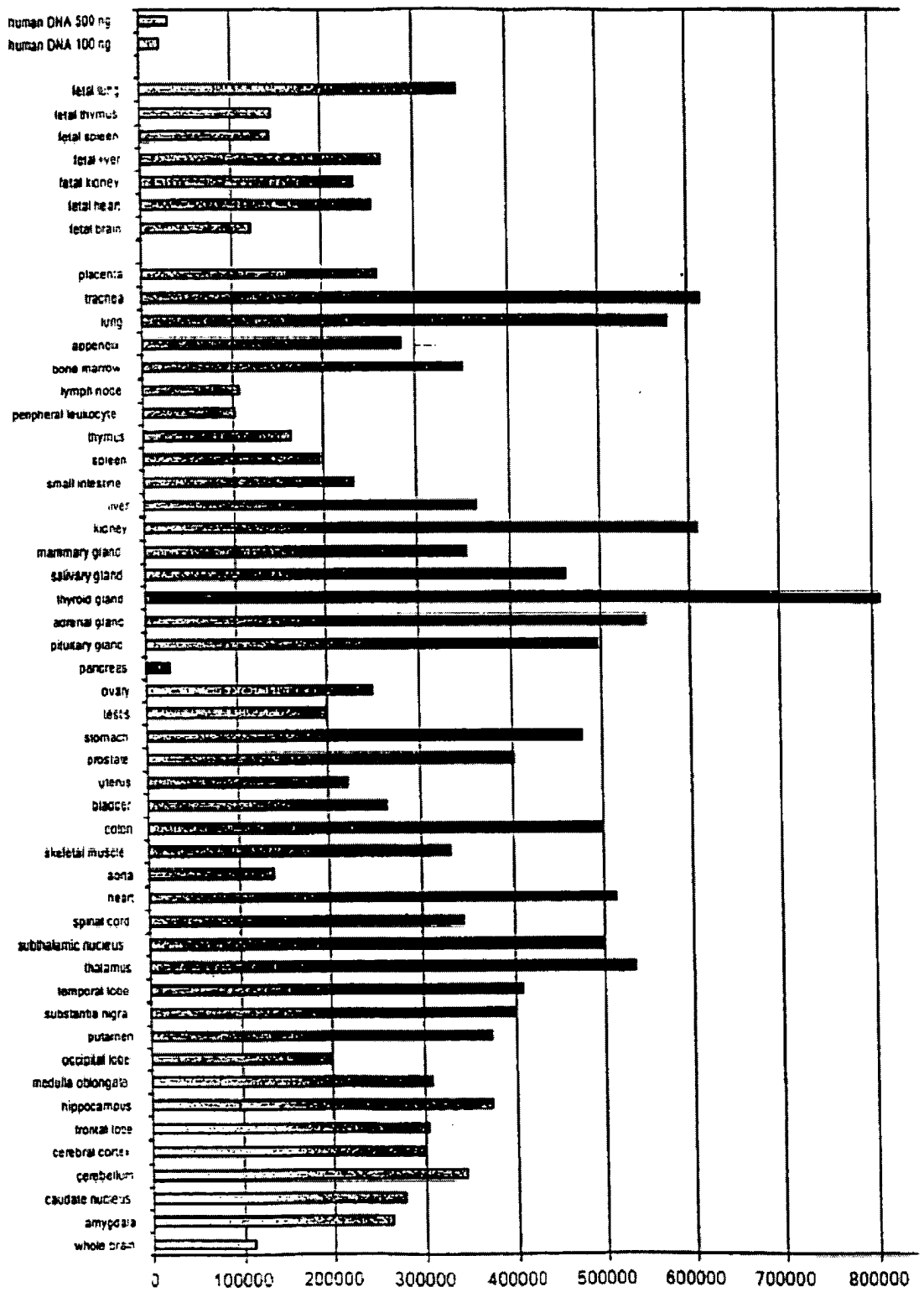

human DNA 500 ng
human DNA 100 ng
fetal liver
fetal thymus
fetal spleen
fetal liver
fetal kidney
fetal heart
fetal brain
placenta
trachea
lung
appendix
bone marrow
lymph node
peripheral leukocyte
thymus
spleen
small intestine
liver
kidney
mammary gland
salivary gland
thyroid gland
adrenal gland
pituitary gland
pancreas
ovary
testis
stomach
prostate
uterus
bladder
colon
skeletal muscle
aorta
heart
spinal cord
subthalamic nucleus
thalamus
temporal lobe
substantia nigra
putamen
occipital lobe
medulla oblongata
hippocampus
frontal lobe
cerebral cortex
cerebellum
caudate nucleus
amygdala
whole brain
0
100000
200000
300000
400000
500000
600000
700000
800000
B18 mRNA (arbitrary units)

FIG.1

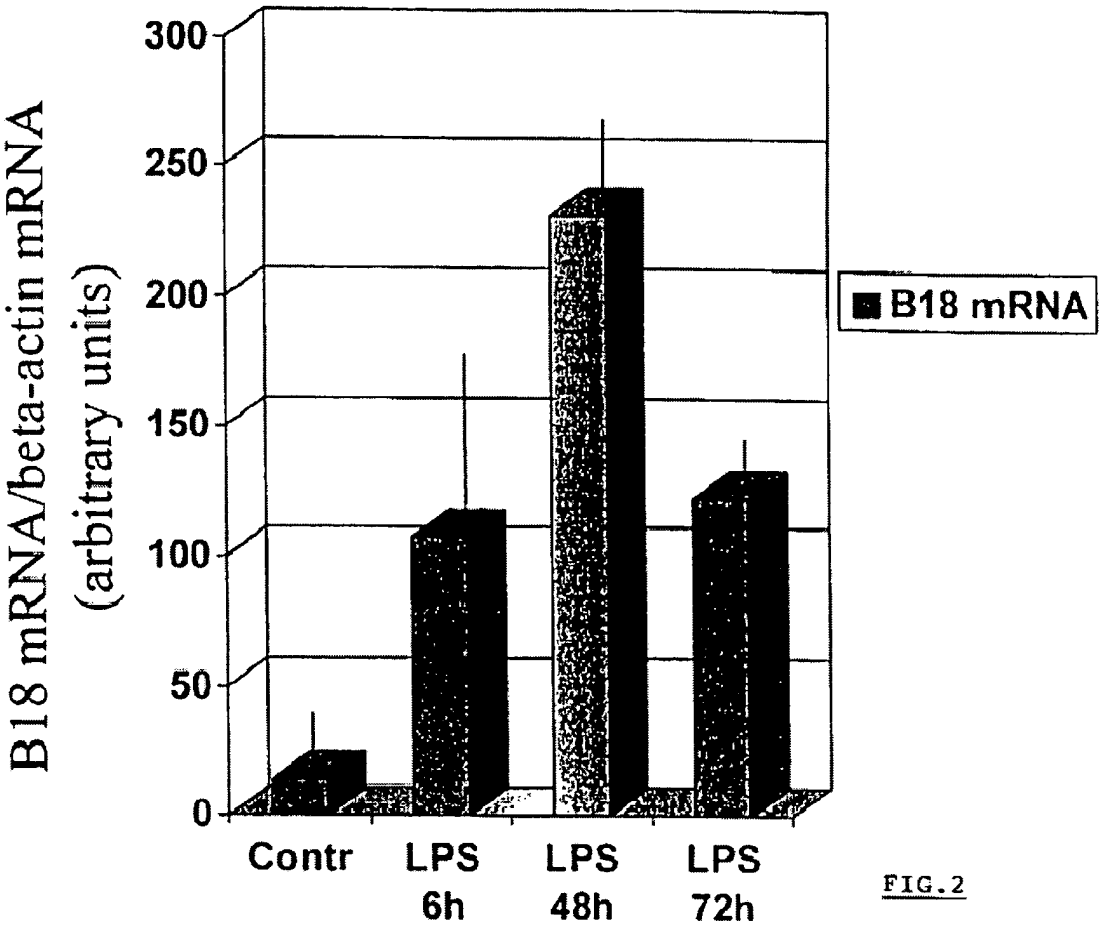

B18 mRNA/beta-actin mRNA
(arbitrary units)
300
250
200
150
100
50
0
Contr
LPS 6h
LPS 48h
LPS 72h
B18 mRNA

FIG.2

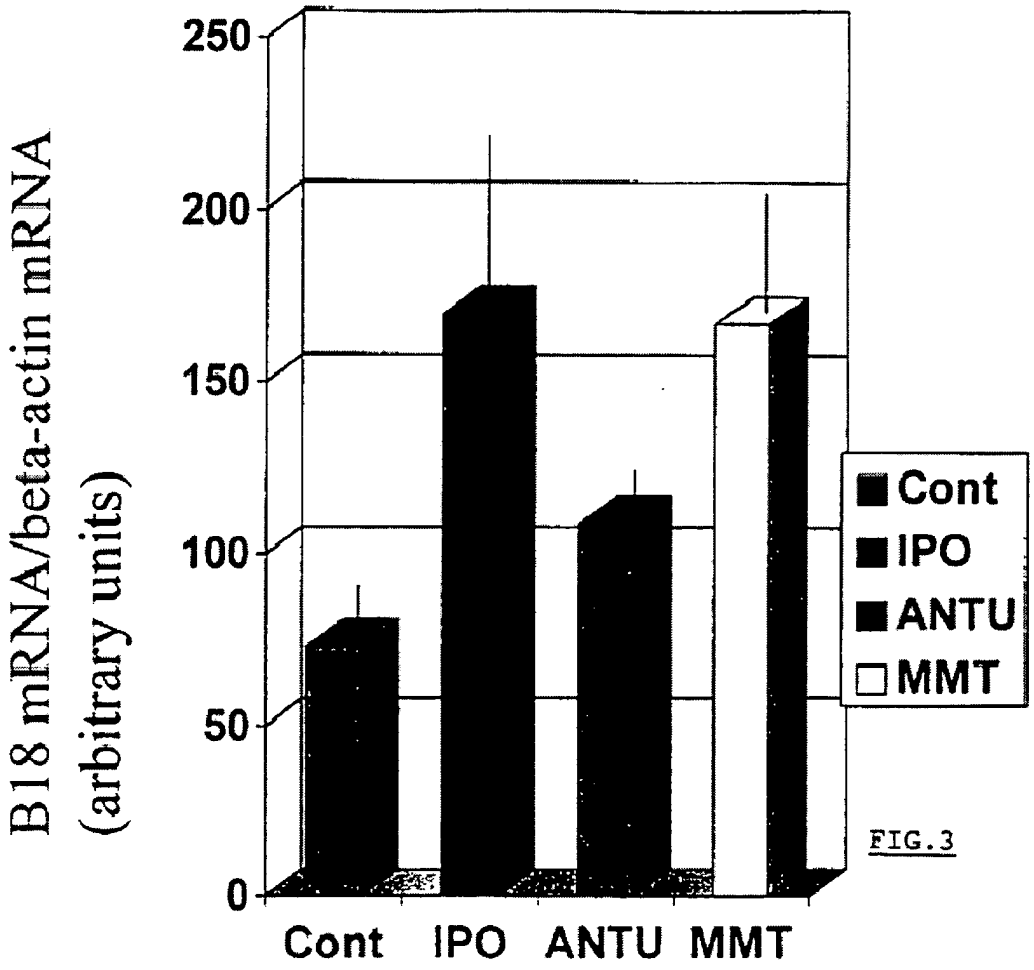

B18 mRNA/beta-actin mRNA
(arbitrary units)
250
200
150
100
50
0
Cont
IPO
ANTU
MMT
Cont
IPO
ANTU
MMT

FIG.3

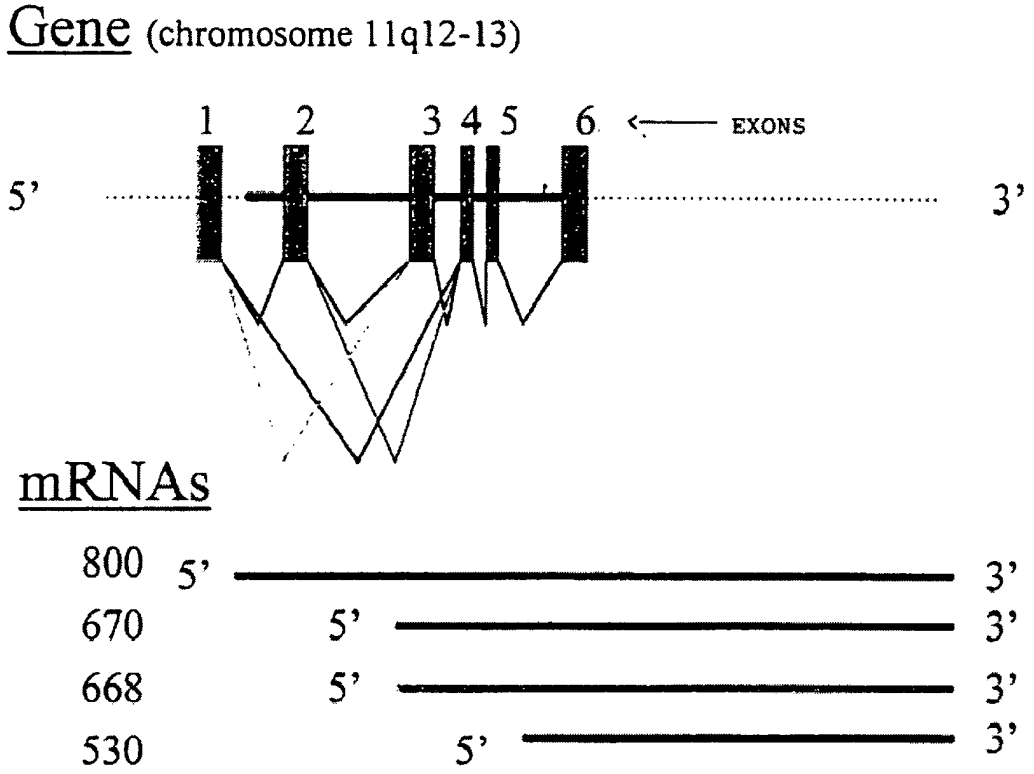

Gene (chromosome 11q12-13)
1 2 3 4 5 6
EXONS
5'
3'
mRNAs
800
670
668
530
Proteins
ATPase-β
A.O.
PRX
17 kDa
12.3 kDa
12.3 kDa
7.7 kDa

FIG.4

CLUSTAL V alignment of human and rat B18 amino acid sequences (Identity: 90%, Homology: 97.5%):

```
B18hum      MAPIKVGDAIPAVEVFEGEPGNKVNLAELFKGKKGVLFGVPGAFTPGCSK = SEQIDNO1
B18rat      MAPIKVGDTIPSVEVFEGEPGKKVNLAELFKDKKGVLFGVPGAFTPGCSK
            ********.**.*********.*********.******************

B18hum      THLPGFVEQAEALKAKGVQVVACLSVNDAFVTGEWGRAHKAEGKVRLLAD
B18rat      THLPGFVEQAGALKAKGAQVVACLSVNDVFVTAEWGRAHQAEGKVQLLAD
            ********** ****** ********** ***.******.*****.****

B18hum      PTGAFGKETDLLLDDSLVSIFGNRRLKRFSMVVQDGIVKALNVEPDGTGL
B18rat      PTGAFGKETDLLLDDSLVSLFGNRRLKRFSMVIDKGVVKALNVEPDGTGL
            ******************.************.. *.**************

B18hum      TCSLAPNIISQL
B18rat      TCSLAPNILSQL
            ********.***
```

FIG.5a

CLUSTAL V alignment of human and mouse B18 amino acid sequences (Identity: 91%, Homology: 96%):

```
B18hum      MAPIKVGDAIPAVEVFEGEPGNKVNLAELFKGKKGVLFGVPGAFTPGCSK
B18mouse    MAPIKVGDAIPSVEVFEGEPGKKVNLAELFKGKKGVLFGVPGAFTPGCSK
            ***********.*********.****************************

B18hum      THLPGFVEQAEALKAKGVQVVACLSVNDAFVTGEWGRAHKAEGKVRLLAD
B18mouse    THLPGFVEQAGALKAKGAQVVACLSVNDVFVIEEWGRAHQAEGKVRLLAD
            ********** ****** ********** **  ******.**********

B18hum      PTGAFGKETDLLLDDSLVSIFGNRRLKRFSMVVQDGIVKALNVEPDGTGL
B18mouse    PTGAFGKATDLLLDDSLVSLFGNRRLKRFSMVIDNGIVKALNVEPDGTGL
            ******* **********.***********...**************

B18hum      TCSLAPNIISQL
B18mouse    TCSLAPNILSQL
            ********.***
```

CLUSTAL V alignment of human and rat cDNA sequences (identity: 612/780, 78.5%):

```
B18hum      GCCAGGAGGCGGAGTGGAAGTGGCCGTGGGGCGGGTATGGGACTAGCTGG
B18rat      ---------------TG---------CGTC---------------CTAGGCAG
                          **         ***                ****   *

B18hum      CGTGTGCGCCCTGAGACGCTCAGCGGGCTATATACTCGTCGGTGGGGCCG
B18rat      CATA---GCC---GGA---TCGGTGCTCCGTGCATCGGCTACTTGGAC--
            * *    ***     **    ** * *  *  *  *    *     * ** *

B18hum      GCGGTCAGTCTGCGGCAGCGGCAGCAAGACGGTGCAGTGAAGGAGAGTGG
B18rat      -------GTGCGTGGCAGGCAGAGCAGGCCGG---AAAGGAGCAGGTTGG
                  **  * *****     **** * ***   *  * ** **  ***
```

FIG.5b

```
B18hum      GCGTCTGGCGGGGTCCGCAGTTTCAGCAGAGCCGCTGCAGCCATGGCCCC
B18rat      GAGTGTGGTGGGGCCCGCAGCTTCAGCAGTGCCGCGGTGACTATGGCCCC
            * ** *** **** ****** ******** ***** *   * ********

B18hum      AATCAAGGTGGGAGATGCCATCCCAGCAGTGGAGGTGTTTGAAGGGGAGC
B18rat      GATCAAGGTGGGAGACACCATTCCCTCAGTGGAGGTATTTGAAGGGGAAC
             **************  **** **  ********** ********** *

B18hum      CAGGGAACAAGGTGAACCTGGCAGAGCTGTTCAAGGGCAAGAAGGGTGTG
B18rat      CTGGAAAGAAGGTGAACTTGGCAGAGCTGTTCAAGGACAAGAAAGGTGTT
            * ** ** ********* ****************** ****** *****

B18hum      CTGTTTGGAGTTCCTGGGGCCTTCACCCCTGGATGTTCCAAGACACACCT
B18rat      TTGTTTGGAGTCCCTGGGGCATTTACACCTGGCTGTTCCAAGACCCATCT
             ********** ******** ** ** ***** ********** ** **

B18hum      GCCAGGGTTTGTGGAGCAGGCTGAGGCTCTGAAGGCCAAGGGAGTCCAGG
B18rat      GCCTGGGTTTGTGGAGCAAGCCGGAGCTCTGAAGGCCAAGGGAGCACAAG
            *** ************** ** *  ******************  ** *

B18hum      TGGTGGCCTGTCTGAGTGTTAATGATGCCTTTGTGACTGGCGAGTGGGGC
B18rat      TGGTGGCCTGTCTGAGTGTTAATGATGTCTTCGTGACTGCAGAGTGGGGT
            ***************************** *** *******  ********

B18hum      CGAGCCCACAAGGCGGAAGGCAAGGTTCGGCTCCTGGCTGATCCCACTGG
B18rat      CGAGCCCACCAGGCAGAAGGCAAGGTTCAGCTCCTGGCTGACCCCACTGG
            ********* **** ************ ************ *********

B18hum      GGCCTTTGGGAAGGAGACAGACTTATTACTAGATGATTCGCTGGTGTCCA
B18rat      AGCTTTTGGAAAGGAGACAGATTTACTACTAGATGATTCTTTGGTGTCTC
             ** ***** *********** *** ************  *******

B18hum      TCTTTGGGAATCGACGTCTCAAGAGGTTCTCCATGGTGGTACAGGATGGC
B18rat      TCTTTGGGAATCGTCGGCTAAAAAGGTTCTCCATGGTGATAGACAAGGGC
            ************ ** ** ** *************** ** *  * ***

B18hum      ATAGTGAAGGCCCTGAATGTGGAACCAGATGGCACAGGCCTCACCTGCAG
B18rat      GTAGTAAAGGCACTGAACGTGGAGCCGGATGGCACAGGCCTCACCTGCAG
             **** ***** ***** ***** ** ************************

B18hum      CCTGGCACCCAATATCATCTCACAGCTCTGAGGCCCTGGGCCAGATTACT
B18rat      CCTGGCCCCCAACATCCTCTCACAACTCTGAGGCCCTGA-CCAGA--ATG
            ****** ***** *** ******* ************  *****  *

B18hum      TCCTCCACCCCTCCCTATCTCACCTGCCCAGCCCTGTGCTGG-GGCCCTG
B18rat      TCCTCTGACTCTCCC-ATCTCCTCCACCCAGCTCTGGGCCAAAGGCCCAG
            *****   * ***** *****  *  ****** *** **    ***** *

B18hum      CA------------------ATTGGAATG-----TTGGCCAGATTTCTGC
B18rat      TACCTCCTTACCTGAGGGCCACTGGAATGGAACCTTGACAATATTTCTGC
             *                  * *******     *** * * ********

B18hum      AATAAACACTTGTGGTTTGCGGAAAAAAA----------
B18rat      AATAAACAGTT-TAATTTGTGAAAAAAAAAAAAAAAAAAA
            ******** ** *  **** * *******
```

CLUSTAL V alignment of human and mouse cDNA sequences (Identity: 552/675, 81.8%):

FIG.5c

```
B18hum          GCCAGGAGGCGGAGTGGAAGTGGCCGTGGGGCGGGTATGGGACTAGCTGG
B18mouse        -------------------------------------------------

B18hum          CGTGTGCGCCCTGAGACGCTCAGCGGGCTATATACTCGTCGGTGGGGCCG
B18mouse        ----------------TGCTCCGTG----------CATCGACGTGCTTG

B18hum          GCGGTCAGTCTGCGGCAGCGGCAGCAAGACGGTGCAGTGAAGGAGAGTGG
B18mouse        GCAGGCAG-------------AGCAGGCCGG---AAAGAAGCAGGTTGG

B18hum          GCGTCTGGCGGGGTCCGCAGTTTCAGCAGAGCCGCTGCAGCCATGGCCCC
B18mouse        GAGTGTGGCGGAGCCCGCAGCTTCAGCAGCTCCGCGGTGACCATGGCCCC

B18hum          AATCAAGGTGGGAGATGCCATCCCAGCAGTGGAGGTGTTTGAAGGGGAGC
B18mouse        GATCAAGGTGGGAGATGCCATTCCCTCAGTGGAGGTATTTGAAGGGGAAC

B18hum          CAGGGAACAAGGTGAACCTGGCAGAGCTGTTCAAGGGCAAGAAGGGTGTG
B18mouse        CGGGAAAGAAGGTGAACTTGGCAGAGCTGTTCAAGGGCAAGAAAGGTGTT

B18hum          CTGTTTGGAGTTCCTGGGGCCTTCACCCCTGGATGTTCCAAGACACACCT
B18mouse        TTGTTTGGAGTCCCTGGGGCATTTACACCTGGCTGTTCTAAGACCCACCT

B18hum          GCCAGGGTTTGTGGAGCAGGCTGAGGCTCTGAAGGCCAAGGGAGTCCAGG
B18mouse        GCCTGGGTTTGTGGAGCAAGCTGGAGCTCTGAAGGCTAAGGGAGCGCAGG

B18hum          TGGTGGCCTGTCTGAGTGTTAATGATGCCTTTGTGACTGGCGAGTGGGGC
B18mouse        TGGTGGCCTGTCTGAGCGTTAATGACGTCTTTGTGATTGAAGAGTGGGGT

B18hum          CGAGCCCACAAGGCGGAAGGCAAGGTTCGGCTCCTGGCTGATCCCACTGG
B18mouse        CGAGCCCACCAGGCAGAAGGCAAGGTTCGGCTCCTGGCTGACCCCACTGG

B18hum          GGCCTTTGGGAAGGAGACAGACTTATTACTAGATGATTCGCTGGTGTCCA
B18mouse        AGCCTTTGGGAAGGCGACAGACTTATTATTGGATGATTCTTTGGTGTCTC

B18hum          TCTTTGGGAATCGACGTCTCAAGAGGTTCTCCATGGTGGTACAGGATGGC
B18mouse        TCTTTGGGAATCGTCGGCTGAAAAGGTTCTCCATGGTGATAGACAACGGC

B18hum          ATAGTGAAGGCCCTGAATGTGGAACCAGATGGCACAGGCCTCACCTGCAG
B18mouse        ATAGTGAAGGCACTGAACGTGGAGCCAGATGGCACAGGCCTCACCTGCAG

B18hum          CCTGGCACCCAATATCATCTCACAGCTCTGAGGCCCTGGGCCAGATTACT
B18mouse        CCTGGCCCCCAACATCCTCTCCCAACTCTGAGGCCCTGG-CCAGATG---

B18hum          TCCTCCACCCCTCCCTATCTCACCTGCCCAGCCCTGTGCTGGGGCCCTGC
B18mouse        TCCTCTGACTCTCCC-ATCTCTCCCACCCGGCTCT------AGGCC----

B18hum          AATTGGAATGTTGGCCAGATTTCTGCAATAAACACTTGTGGTTTGCGGAA
B18mouse        ----AAAAGGCTCGGTACCTCCTTACTGGGAGC-CACGT----------
```

Fig. 6.

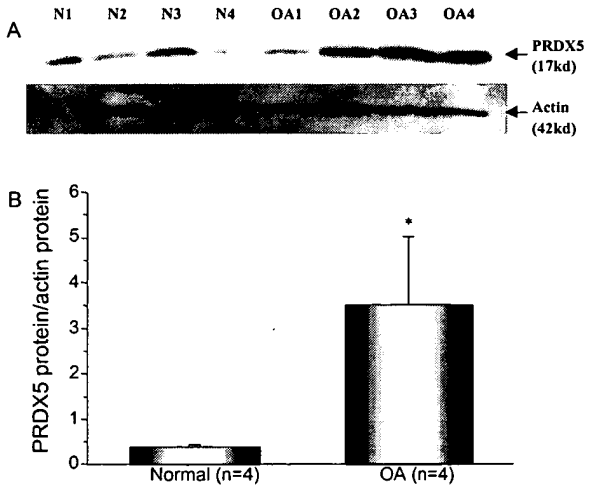

A
N1
N2
N3
N4
OA1
OA2
OA3
OA4
PRDX5 (17kd)
Actin (42kd)
B
PRDX5 protein/actin protein
0
1
2
3
4
5
6
*
Normal (n=4)
OA (n=4)

Fig . 7.

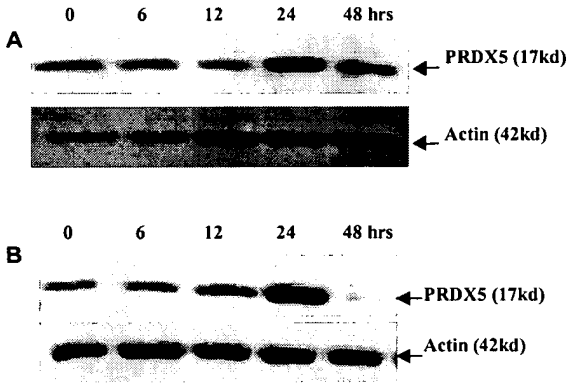

A
0
6
12
24
48 hrs
PRDX5 (17kd)
Actin (42kd)
B
0
6
12
24
48 hrs
PRDX5 (17kd)
Actin (42kd)

Fig. 8.

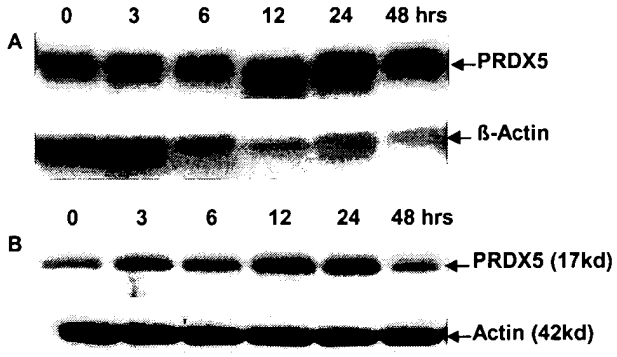
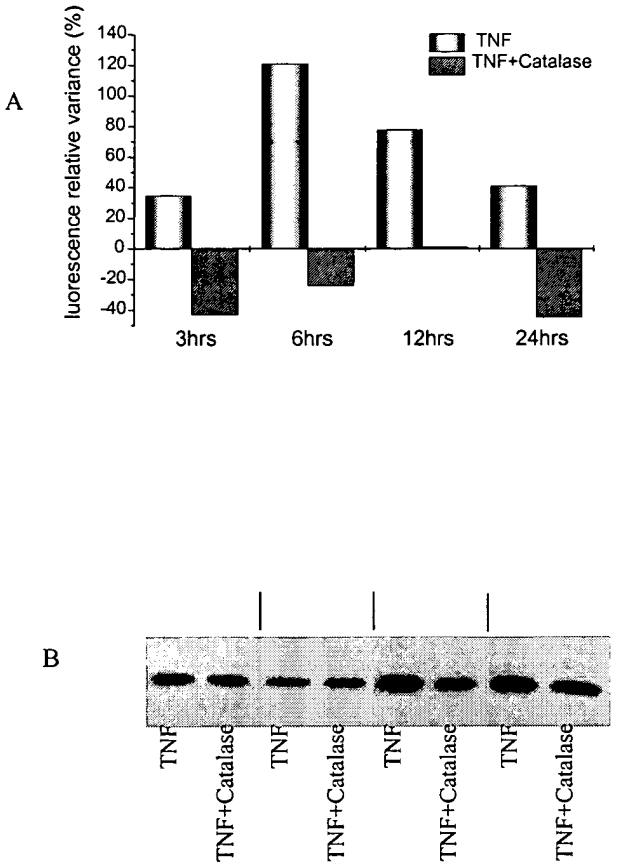

A
0 3 6 12 24 48 hrs
PRDX5
ß-Actin
B
0 3 6 12 24 48 hrs
PRDX5 (17kd)
Actin (42kd)

Fig. 9.


A
luorescence relative variance (%)
140
120
100
80
60
40
20
0
-20
-40
TNF
TNF+Catalase
3hrs
6hrs
12hrs
24hrs
B
TNF
TNF+Catalase
TNF
TNF+Catalase
TNF
TNF+Catalase
TNF
TNF+Catalase

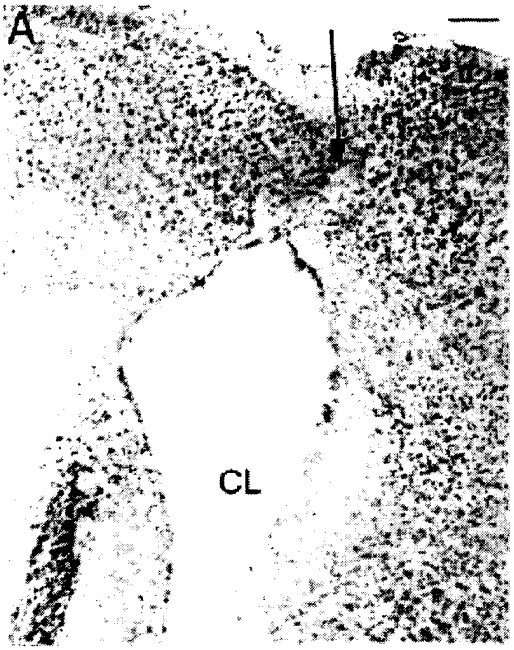


Fig. 10

Fig. 11

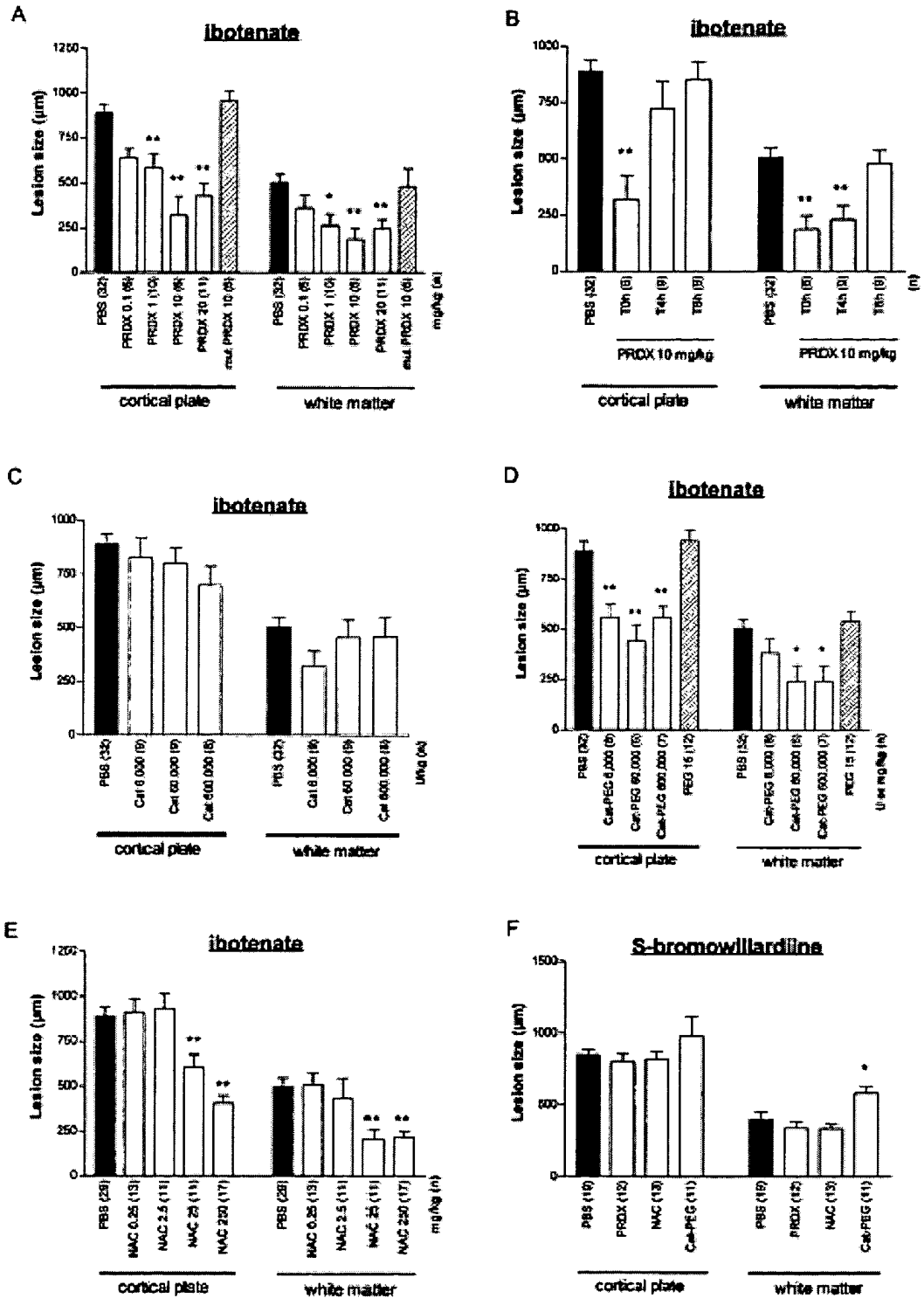

A
Ibotenate
Lesion size (µm)
cortical plate
white matter
B
Ibotenate
Lesion size (µm)
PRDX 10 mg/kg
cortical plate
white matter
C
Ibotenate
Lesion size (µm)
cortical plate
white matter
D
Ibotenate
Lesion size (µm)
cortical plate
white matter
E
Ibotenate
Lesion size (µm)
cortical plate
white matter
F
S-bromowillardiine
Lesion size (µm)
cortical plate
white matter

Fig. 12

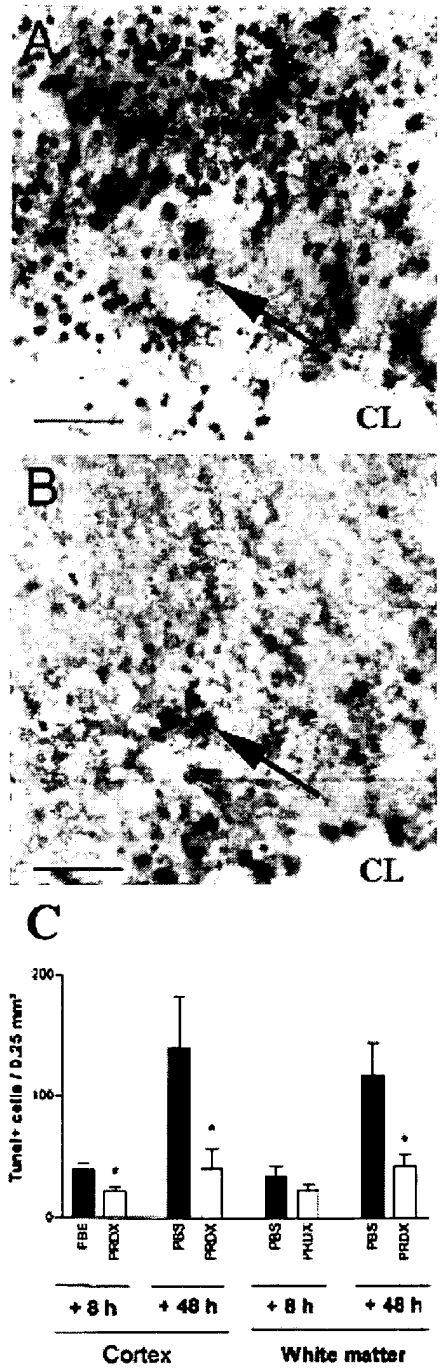
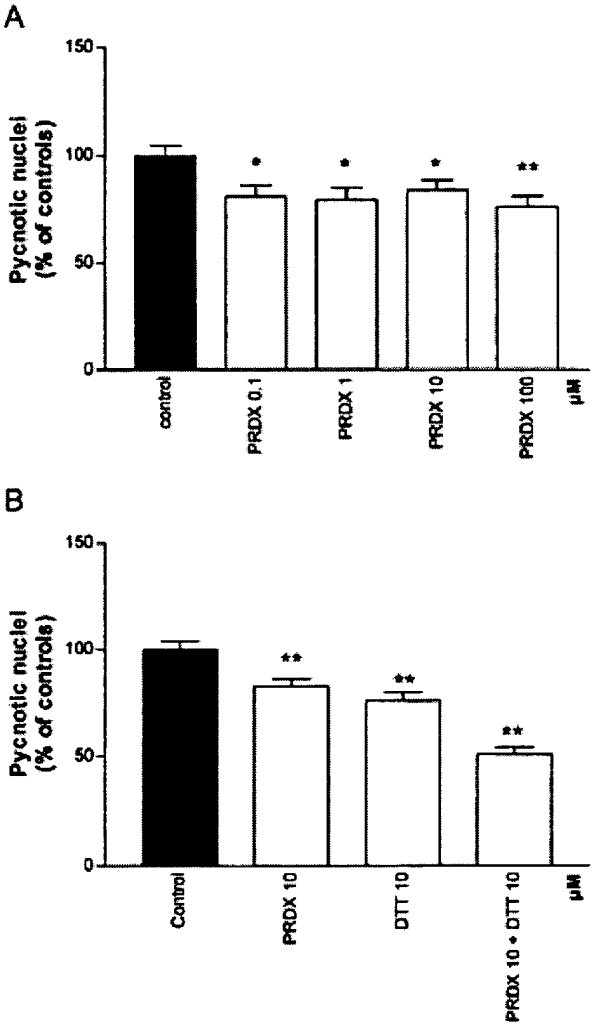

A
CL
B
CL
C
Tunel+ cells / 0.25 mm²
200
100
0
FBS
PRDX
PBS
PRDX
PBS
PHUX
PBS
PRDX
+ 8 h
+ 48 h
+ 8 h
+ 48 h
Cortex
White matter

Fig. 13


A
Pycnotic nuclei (% of controls)
150
100
50
0
*
*
*
**
control
PRDX 0.1
PRDX 1
PRDX 10
PRDX 100
µM
B
Pycnotic nuclei (% of controls)
150
100
50
0
**
**
**
Control
PRDX 10
DTT 10
PRDX 10 + DTT 10
µM

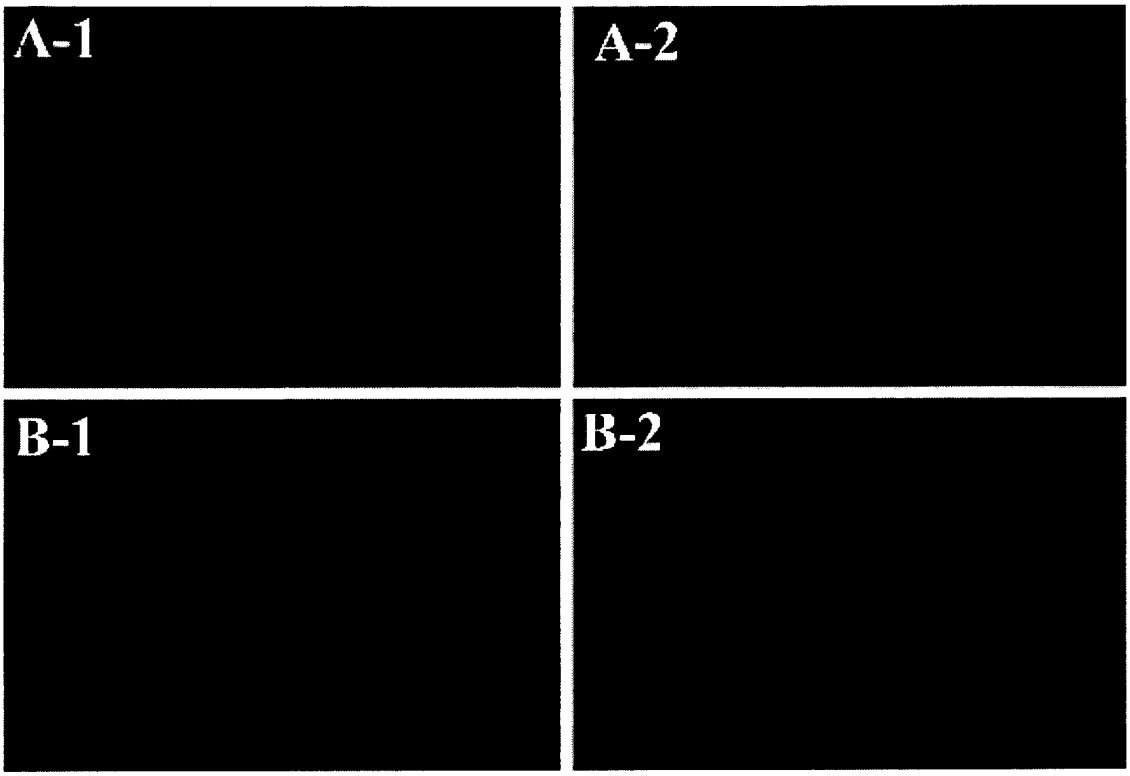



Fig. 14